GenCore version 4.5

OM protein - protein search, using sw model

Run on: August 13, 2001, 11:23:05 ; Search time 110.38 Seconds
(without alignments)
1.648 Million cell updates/sec

Title: PCT-US00-40496-12
Perfect score: 3
Sequence: 1 KRR 3

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 412676 seqs, 60623988 residues

Word size : 0

Total number of hits satisfying chosen parameters: 158286

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : A_Geneseq_0601:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3	100.0	4	18	AAW26211	Fusion protein hyd
2	3	100.0	4	19	AAW52421	Beta-turn region u
3	3	100.0	4	20	AAY06089	Archvillin nuclear
4	3	100.0	4	20	AAY09618	Antimicrobial cycl
5	3	100.0	4	20	AAY15854	Melanocortin recep
6	3	100.0	4	20	AAW95379	IL-1 alpha propiec
7	3	100.0	4	21	AAB12266	Synthetic oligopep
8	3	100.0	4	22	AAB80640	Human glandular ka
9	3	100.0	4	22	AAB80642	Human glandular ka
10	3	100.0	4	22	AAB80643	Human glandular ka
11	3	100.0	4	22	AAB80644	Human glandular ka
12	3	100.0	4	22	AAB80650	Human glandular ka
13	3	100.0	5	15	AAR62390	Phopholipase A2 in
14	3	100.0	5	17	AAR86617	HIV TAT cellular u
15	3	100.0	5	17	AAR86618	HIV TAT cellular u
16	3	100.0	5	17	AAR95443	RA susceptibility
17	3	100.0	5	18	AAW26219	Fusion protein hyd
18	3	100.0	5	18	AAW26220	Fusion protein hyd
19	3	100.0	5	18	AAW26224	Fusion protein hyd
20	3	100.0	5	18	AAW26226	Fusion protein hyd
21	3	100.0	5	18	AAW19167	Isoelectric point
22	3	100.0	5	19	AAY20823	Human neurofilamen
23	3	100.0	5	20	AAY06091	Archvillin nuclear
24	3	100.0	5	20	AAW98055	Streptococcus pyog
25	3	100.0	5	20	AAW98057	Streptococcus agal
26	3	100.0	5	21	AAB11066	S. pyogenes sortas
27	3	100.0	5	21	AAB11068	S. aglactiae sorta
28	3	100.0	5	21	AAB14216	HIV SF162 gp120 cl
29	3	100.0	5	21	AAB14222	HIV US4 gp120 clea
30	3	100.0	5	21	AAY69732	ADP-1/TAR binding
31	3	100.0	5	21	AAY49920	Glycocalyx mimic s
32	3	100.0	5	22	AAB80741	hK2 cleavage site
33	3	100.0	5	22	AAB80743	hK2 cleavage site
34	3	100.0	5	22	AAB80744	hK2 cleavage site
35	3	100.0	5	22	AAB80745	hK2 cleavage site
36	3	100.0	5	22	AAB80746	hK2 cleavage site
37	3	100.0	5	22	AAB80747	hK2 cleavage site
38	3	100.0	5	22	AAB80748	hK2 cleavage site
39	3	100.0	6	4	AAP30312	Sequence encoded b
40	3	100.0	6	11	AAR03074	Immunostimulant pe
41	3	100.0	6	17	AAW12964	HCV NS3 protease s
42	3	100.0	6	18	AAW01642	Solubilising motif
43	3	100.0	6	18	AAW19174	Isoelectric point
44	3	100.0	6	19	AAY20320	Human microtubule
45	3	100.0	6	19	AAW79204	Het-A nucleus-tran

ALIGNMENTS

RESULT 1
AAW26211
ID AAW26211 standard; peptide; 4 AA.
XX
AC AAW26211;
XX
DT 16-MAR-1998 (first entry)
XX
DE Fusion protein hydrophilic spacer peptide SEQ ID NO:22.
XX
KW Fusion protein; hydrophilic spacer; recombinant; expression system;
KW carboxypeptidase.
XX
OS Synthetic.
XX
PN WO9728272-A1.
XX
PD 07-AUG-1997.
XX
PF 31-JAN-1997; 97WO-US01470.
XX
PR 31-JAN-1996; 96US-0595043.
XX
PA (TECH-) TECHNOLOGENE INC.
XX
PI Sgarlato GD;
XX
DR WPI; 1997-402624/37.
XX
PT Recombinant protein expression system for fusion protein production
PT - useful for high quantity production of authentic recombinant
PT proteins
XX
PS Claim 6; Page 127; 194pp; English.

XX
CC A novel recombinant vector has been developed which comprises a
CC nucleotide sequence encoding a fusion protein. The fusion protein
CC comprises three domains joined together in order, from N-terminus to
CC C-terminus, of a first domain comprising a protein of interest, a second
CC domain comprising a hydrophilic spacer and an affinity domain, each
CC domain comprising amino acid residues. The present sequence represents
CC a specifically claimed hydrophilic spacer. The recombinant vector is
CC used for the production of authentic recombinant proteins of interest.
CC The method of the invention is useful for the expression of fusion
CC proteins capable of isolation by affinity chromatography in pro- or
CC eukaryotic cells. This method allows for the efficient cleavage and
CC generation of authentic proteins of interest that do not contain
CC extraneous (i.e. non-naturally occurring) amino acids.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 3; DB 18; Length 4;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRR 3
|||
Db 1 krr 3

RESULT 2
AAW52421
ID AAW52421 standard; peptide; 4 AA.
XX
AC AAW52421;
XX
DT 01-JUL-1998 (first entry)
XX
DE Beta-turn region used in cyclic peptide of the invention.
XX
KW Beta-turn region; cyclic peptide; antimicrobial; disinfectant; therapy;
KW preservative; amphipathic anti-parallel beta-sheet region; plant disease.
XX
OS Synthetic.
XX
PN WO9803192-A1.
XX
PD 29-JAN-1998.
XX
PF 23-JUL-1997; 97WO-US12974.
XX
PR 24-JUL-1996; 96US-0685589.
XX
PA (INTR-) INTRABIOTICS PHARM INC.
XX
PI Chang C, Chen J, Gu L;
XX
DR WPI; 1998-120472/11.
XX
PT New cyclic peptide(s) with antimicrobial activity - contain
PT amphipathic beta-sheet, loop and beta-turn regions, have better
PT activity, bio:availability and protease resistance than linear
PT analogues
XX
PS Claim 3; Page 149; 160pp; English.
XX
CC This sequence represents a beta-turn region used in a peptide of the
CC invention. The peptides are cyclic peptides (I), which have: (a) an
CC amphipathic anti-parallel beta-sheet region (SR), a loop region (LR) and
CC a beta-turn region (TR); (b) a net positive charge at physiological pH;
CC and (c) at least one basic amino acid (aa) in LR or TR. (I) are broad
CC spectrum antimicrobials, specifically for use against E. coli,
CC Pseudomonas aeruginosa, methicillin-resistant Staphylococcus aureus
CC (MRSA), vancomycin-resistant Enterococcus faecium and
CC penicillin-resistant Streptococcus pneumoniae. More generally they are
CC active against Gram-positive or -negative bacteria, fungi, yeast and
CC protozoa. Apart from clinical uses, (I) are also used as disinfectants
CC and preservatives for medical equipment, foods, cosmetics etc., also for
CC treatment of plant diseases. Compared with non-cyclised analogues (i.e.
CC tachyplesin and protegrin type peptides), (I) and are more effective,
CC with better bioavailability and/or serum half-life (increased resistance
CC to proteolysis). They are more suitable for oral administration, can be
CC used at lower doses and are unlikely to induce development of resistant
CC strains.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 3; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRR 3
|||
Db 1 krr 3

RESULT 3
AAY06089
ID AAY06089 standard; Peptide; 4 AA.
XX
AC AAY06089;
XX
DT 16-AUG-1999 (first entry)
XX
DE Archvillin nuclear localisation sequence.
XX
KW Supervillin; archvillin; actin binding protein; apoptosis;
KW cell proliferation; therapy; nuclear localisation sequence; human.
XX
OS Homo sapiens.
XX
PN WO9923213-A1.
XX
PD 14-MAY-1999.
XX
PF 30-OCT-1998; 98WO-US23061.
XX
PR 31-OCT-1997; 97US-0962284.
XX
PA (UYMA-) UNIV MASSACHUSETTS.
XX
PI Luna EJ, Pestonjamasp KN, Pope RK, Wulfkuhle JD;
XX
DR WPI; 1999-313338/26.
XX
PT Actin-binding proteins supervillin and archvillin
XX
PS Example 9; Page 76; 118pp; English.
XX
CC This sequence represents a predicted nuclear localisation sequence
CC located at amino acid residues 714-717 of human archvillin (see
CC AAY06079), the muscle isoform of supervillin, which is a novel
CC actin binding protein of the plasma membrane. Supervillins
CC function to block apoptosis in sub-confluent epithelial cells. The
CC invention provides supervillin polypeptides (see AAY06077-79) and
CC polynucleotides (see AAX58619-21), antibodies and modulators of
CC supervillin expression or activity. These are used for diagnosis
CC and treatment of disease, and for inducing apoptosis in cells.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 3; DB 20; Length 4;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRR 3
|||

XX
CC The present invention relates to a peptide comprising an amino acid
CC sequence having a cleavage site specific for an enzyme having a
CC proteolytic activity of human kallikrein 2 (hK2), and which is up to
CC 20 amino acids in length. The invention is useful for producing a
CC prodrug which involves linking a drug which contains a primary amine
CC to the peptide, in which the linking of the peptide to the drug
CC inhibits the therapeutic activity of the drug.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 5; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKKRR 5
|||||
Db 1 gkkrr 5

RESULT 2
AAB80669
ID AAB80669 standard; peptide; 7 AA.
XX
AC AAB80669;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human glandular kallikrein 2 cleavage site peptide #30.
XX
KW Cleavage; kallikrein 2; hK2; prodrug.
XX
OS Synthetic.
XX
PN WO200109165-A2.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-US40496.
XX
PR 29-JUL-1999; 99US-0146316.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Denmeade SR, Isaacs JT, Lilja H, Christensen SB;
XX
DR WPI; 2001-191450/19.
XX
PT New peptides containing cleavage sites specifically cleaved by human
PT kallikrein 2, useful for producing prodrugs which treat hK2-producing
PT cell proliferative disorders without exhibiting non-specific toxicity
PT -
XX
PS Disclosure; Page 8; 38pp; English.
XX
CC The present invention relates to a peptide comprising an amino acid
CC sequence having a cleavage site specific for an enzyme having a
CC proteolytic activity of human kallikrein 2 (hK2), and which is up to
CC 20 amino acids in length. The invention is useful for producing a
CC prodrug which involves linking a drug which contains a primary amine
CC to the peptide, in which the linking of the peptide to the drug
CC inhibits the therapeutic activity of the drug.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 5; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKKRR 5
|||||
Db 2 gkkrr 6

RESULT 3
AAB80706
ID AAB80706 standard; peptide; 7 AA.
XX
AC AAB80706;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human glandular kallikrein 2 substrate peptide #36.
XX
KW Cleavage; kallikrein 2; hK2; prodrug.
XX
OS Synthetic.
XX
PN WO200109165-A2.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-US40496.
XX
PR 29-JUL-1999; 99US-0146316.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Denmeade SR, Isaacs JT, Lilja H, Christensen SB;
XX
DR WPI; 2001-191450/19.
XX
PT New peptides containing cleavage sites specifically cleaved by human
PT kallikrein 2, useful for producing prodrugs which treat hK2-producing
PT cell proliferative disorders without exhibiting non-specific toxicity
PT -
XX
PS Example 8; Page 29; 38pp; English.
XX
CC The present invention relates to a peptide comprising an amino acid
CC sequence having a cleavage site specific for an enzyme having a
CC proteolytic activity of human kallikrein 2 (hK2), and which is up to
CC 20 amino acids in length. The invention is useful for producing a
CC prodrug which involves linking a drug which contains a primary amine
CC to the peptide, in which the linking of the peptide to the drug
CC inhibits the therapeutic activity of the drug.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 5; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKKRR 5
|||||
Db 2 gkkrr 6

RESULT 4
AAW59284
ID AAW59284 standard; Protein; 12 AA.
XX
AC AAW59284;
XX
DT 11-SEP-1998 (first entry)
XX
DE Homo sapiens adrenal corticotrophic hormone urokinase cleavage site.
XX
KW adrenal corticotrophic hormone; proprotein; protease-activatable;
KW cancer; specific; selective; treatment; urokinase; cleavage site.
XX
OS Homo sapiens.
XX

```
PN   WO9820135-A2.
XX
PD   14-MAY-1998.
XX
PF   05-NOV-1997;   97WO-US20207.
XX
PR   06-NOV-1996;   96US-0030376.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Fitzgerald DJ,  Pastan I,  Reiter Y;
XX
DR   WPI; 1998-286951/25.
XX
PT   Pseudomonas exotoxin A-like proprotein which is protease-activatable
PT   - allows activation by desired protease through protease activatable
PT   sequence in domain II loop, useful to selectively kill e.g. cancer
PT   cells
XX
PS   Disclosure; Page 29; 74pp; English.
XX
CC   The sequence is that of an adrenal corticotrophic hormone urokinase
CC   cleavage site which was used in construction of a protease-activatable
CC   Pseudomonas exotoxin (PE) A-like proprotein. Such proproteins
CC   can be used to kill (especially prostate or colon) cancer
CC   cells. They are modified for activation by a desired protease
CC   by insertion of a protease activatable sequence in the domain
CC   II loop; proprotein activation results in formation of cytotoxic
CC   PE. PE is normally translocated into the cytosol after cleavage of a
CC   furin recognition site in domain II by furin, but in the proproteins the
CC   furin recognition site is replaced by a site recognised by a protease
CC   made/secreted by a cell targeted for death, e.g. a cancer cell. The
CC   proproteins can be used in vivo e.g. to treat mammals suffering from
CC   cancer or ex vivo e.g. to selectively eliminate cultured
CC   mammalian cells prior to reintroduction.  Mammalian cells can be
CC   engineered to exhibit altered susceptibility to a specific proprotein
CC   or to produce proprotein e.g. for gene therapy. Activation by a target
CC   protease rather than furin allows toxicity to be more cell-specific
CC   than for PE. The proproteins also provide more specific cancer
CC   treatment than previous immunotoxin-based therapies.
XX
SQ   Sequence   12 AA;

  Query Match             100.0%;  Score 5;  DB 19;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKKRR 5
           |||||
Db       3 gkkrr 7


RESULT   5
AAW59285
ID   AAW59285 standard; Protein; 12 AA.
XX
AC   AAW59285;
XX
DT   11-SEP-1998  (first entry)
XX
DE   Homo sapiens adrenal corticotrophic hormone urokinase cleavage site.
XX
KW   adrenal corticotrophic hormone; proprotein; protease-activatable;
KW   cancer; specific; selective; treatment; urokinase; cleavage site.
XX
OS   Homo sapiens.
XX
PN   WO9820135-A2.
XX
PD   14-MAY-1998.
XX
PF   05-NOV-1997;   97WO-US20207.
XX
PR   06-NOV-1996;   96US-0030376.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Fitzgerald DJ,  Pastan I,  Reiter Y;
XX
DR   WPI; 1998-286951/25.
XX
PT   Pseudomonas exotoxin A-like proprotein which is protease-activatable
PT   - allows activation by desired protease through protease activatable
PT   sequence in domain II loop, useful to selectively kill e.g. cancer
PT   cells
XX
PS   Disclosure; Page 29; 74pp; English.
XX
CC   The sequence is that of an adrenal corticotrophic hormone urokinase
CC   cleavage site which was used in construction of a protease-activatable
CC   Pseudomonas exotoxin (PE) A-like proprotein. Such proproteins
CC   can be used to kill (especially prostate or colon) cancer
CC   cells. They are modified for activation by a desired protease
CC   by insertion of a protease activatable sequence in the domain
CC   II loop; proprotein activation results in formation of cytotoxic
CC   PE. PE is normally translocated into the cytosol after cleavage of a
CC   furin recognition site in domain II by furin, but in the proproteins the
CC   furin recognition site is replaced by a site recognised by a protease
CC   made/secreted by a cell targeted for death, e.g. a cancer cell. The
CC   proproteins can be used in vivo e.g. to treat mammals suffering from
CC   cancer or ex vivo e.g. to selectively eliminate cultured
CC   mammalian cells prior to reintroduction.  Mammalian cells can be
CC   engineered to exhibit altered susceptibility to a specific proprotein
CC   or to produce proprotein e.g. for gene therapy. Activation by a target
CC   protease rather than furin allows toxicity to be more cell-specific
CC   than for PE. The proproteins also provide more specific cancer
CC   treatment than previous immunotoxin-based therapies.
XX
SQ   Sequence   12 AA;

  Query Match             100.0%;  Score 5;  DB 19;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GKKRR 5
           |||||
Db       4 gkkrr 8


RESULT   6
AAW59286
ID   AAW59286 standard; Protein; 12 AA.
XX
AC   AAW59286;
XX
DT   11-SEP-1998  (first entry)
XX
DE   Homo sapiens adrenal corticotrophic hormone urokinase cleavage site.
XX
KW   adrenal corticotrophic hormone; proprotein; protease-activatable;
KW   cancer; specific; selective; treatment; urokinase; cleavage site.
XX
OS   Homo sapiens.
XX
PN   WO9820135-A2.
XX
PD   14-MAY-1998.
XX
PF   05-NOV-1997;   97WO-US20207.
XX
PR   06-NOV-1996;   96US-0030376.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
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```
OS   Synthetic.
XX
PN   WO200077193-A1.
XX
PD   21-DEC-2000.
XX
PF   09-JUN-2000; 2000WO-NL00399.
XX
PR   10-JUN-1999;   99EP-0201846.
PR   10-JUN-1999;   99US-0138443.
XX
PA   (UYGR-) RIJKSUNIV GRONINGEN.
XX
PI   Quax WJ,  Verhaert RMD,  Beekwilder MJ,  Aehle W;
XX
DR   WPI; 2001-112224/12.
DR   N-PSDB; AAF23957.
XX
PT   Selecting an enzyme with desired catalytic activity, useful as
PT   catalysts in specific reactions, comprises selecting for display
PT   vehicle carrying nucleic acid encoding a mutant enzyme with a mutated
PT   site other than its catalytic site
XX
PS   Example 4; Page 33; 52pp; English.
XX
CC   The present sequence was generated and used in an example to demonstrate
CC   a method for selecting an enzyme mutant with desired catalytic activity.
CC   The method comprises displaying each of the enzyme mutants on a display
CC   vehicle surface containing a nucleic acid encoding the mutant; and
CC   selecting for a display vehicle carrying a nucleic acid encoding a mutant
CC   enzyme with at least a mutated site other than its catalytic site. The
CC   method is useful for selecting or obtaining enzymes with a desired
CC   activity. Such enzymes are used as catalysts that accelerate the rate of
CC   specific reactions in industry, in food processing, in the manufacture of
CC   laundry soap, and in the production of fine (bio)chemicals.
XX
SQ   Sequence   7 AA;

  Query Match             100.0%;  Score 5;  DB 22;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GAKRR 5
           |||||
Db       2 gakrr 6


RESULT   5
AAY26298
ID   AAY26298 standard; Peptide; 12 AA.
XX
AC   AAY26298;
XX
DT   03-NOV-1999  (first entry)
XX
DE   Peptide-6 derived from murine NFAT1.
XX
KW   Murine NFAT1 protein; NFAT dephosphorylation; NFAT protein; calcineurin;
KW   antibody; immunisation. transcription factor;
KW   calcineurin-mediated dephosphorylation.
XX
OS   Mus musculus.
XX
PN   WO9940930-A1.
XX
PD   19-AUG-1999.
XX
PF   11-FEB-1999;   99WO-US03085.
XX
PR   12-FEB-1998;   98US-0074467.
XX
PA   (BLOO-) CENT BLOOD RES INC.
XX
PI   Aramburu J,  Hogan PG,  Rao A;
XX
DR   WPI; 1999-508578/42.
XX
PT   Inhibitors of NFAT activation by calcineurin, used to, e.g. treat a
PT   disease involving hyperactivity
XX
PS   Disclosure; Page 117; 125pp; English.
XX
CC   The present sequence is a peptide derived from murine NFAT1 protein
CC   (239 to 255). This is used to determine dephosphorylation of NFAT by
CC   examining specific sites remaining phosphorylated in the NFAT protein
CC   after treatment with calcineurin. The presence or absence of covalently
CC   bound phosphate is determined using antibodies, or a functionally
CC   equivalent reagent, that discriminate between phosphorylated and
CC   unphosphorylated forms of a specific peptide in the context of the
CC   larger protein  or protein fragment. Antibodies to phosphorylated or
CC   dephosphorylated NFAT peptides can be raised, e.g., by immunisation of
CC   rabbits.
XX
SQ   Sequence   12 AA;

  Query Match             100.0%;  Score 5;  DB 20;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GAKRR 5
           |||||
Db       8 gakrr 12


RESULT   6
AAY26299
ID   AAY26299 standard; Peptide; 17 AA.
XX
AC   AAY26299;
XX
DT   03-NOV-1999  (first entry)
XX
DE   Peptide comprising residues 239 to 255 of murine NFAT1.
XX
KW   Murine NFAT1 protein; NFAT dephosphorylation; NFAT protein; calcineurin;
KW   antibody; immunisation. transcription factor;
KW   calcineurin-mediated dephosphorylation.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..12
FT                   /note= "Peptide-4"
FT   Peptide         4..13
FT                   /note= "Peptide-5"
FT   Peptide         6..17
FT                   /note= "Peptide-6"
XX
PN   WO9940930-A1.
XX
PD   19-AUG-1999.
XX
PF   11-FEB-1999;   99WO-US03085.
XX
PR   12-FEB-1998;   98US-0074467.
XX
PA   (BLOO-) CENT BLOOD RES INC.
XX
PI   Aramburu J,  Hogan PG,  Rao A;
XX
DR   WPI; 1999-508578/42.
XX
PT   Inhibitors of NFAT activation by calcineurin, used to, e.g. treat a
PT   disease involving hyperactivity
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: August 13, 2001, 11:25:08 ; Search time 110.38 Seconds
(without alignments)
1.648 Million cell updates/sec

Title: PCT-US00-40496-13
Perfect score: 3
Sequence: 1 SRR 3

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 412676 seqs, 60623988 residues

Word size : 0

Total number of hits satisfying chosen parameters: 158286

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

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21: /cgn1_9/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22: /cgn1_9/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3	100.0	4	18	AAW11147	CD4 peptide capabl
2	3	100.0	4	20	AAY23396	V beta 6 clone fou
3	3	100.0	4	22	AAB80641	Human glandular ka
4	3	100.0	4	22	AAB80651	Human glandular ka
5	3	100.0	4	22	AAB30780	Peptide which is u
6	3	100.0	5	17	AAW00250	Subtilisin N62D/G1
7	3	100.0	5	19	AAY20459	Human microtubule
8	3	100.0	5	19	AAW65358	Peptide #19 useful
9	3	100.0	5	19	AAW65359	Peptide #20 useful
10	3	100.0	5	19	AAW65360	Peptide #21 useful
11	3	100.0	5	20	AAW98066	Sorting signal cha
12	3	100.0	5	20	AAW98063	Staphylococcal pro
13	3	100.0	5	21	AAB11074	S. apyogenes sorta
14	3	100.0	5	21	AAB11077	S. pyogenes sortas
15	3	100.0	5	21	AAB37745	Fibronectin-derive
16	3	100.0	5	21	AAB37746	Fibronectin-derive
17	3	100.0	5	21	AAB37747	Fibronectin-derive
18	3	100.0	5	21	AAY80742	Fibroblast invasio
19	3	100.0	5	21	AAY80743	Fibroblast invasio
20	3	100.0	5	21	AAY80744	Fibroblast invasio
21	3	100.0	5	21	AAY58448	Staphylococcus aur
22	3	100.0	5	22	AAB80742	hK2 cleavage site
23	3	100.0	5	22	AAB69521	Staphylococcus aur
24	3	100.0	6	15	AAR55741	dsRNA-dependent ki
25	3	100.0	6	17	AAW03507	Alpha(v)-Beta(3) i
26	3	100.0	6	18	AAW11148	CD4 peptide capabl
27	3	100.0	6	19	AAW56835	Enzyme inhibitor p
28	3	100.0	6	19	AAW56836	Enzyme inhibitor p
29	3	100.0	6	19	AAW56943	Enzyme inhibitor p
30	3	100.0	6	19	AAW56945	Enzyme inhibitor p
31	3	100.0	6	19	AAW57034	Enzyme inhibitor p
32	3	100.0	6	19	AAW56918	Enzyme inhibitor p
33	3	100.0	6	19	AAW56960	Enzyme inhibitor p
34	3	100.0	6	20	AAY33940	Immunogenic myosta
35	3	100.0	6	20	AAY23501	V beta 6 clone fou
36	3	100.0	6	20	AAY21585	Integrin-binding p
37	3	100.0	6	21	AAB22064	dsRNS kinase pp68
38	3	100.0	6	21	AAB22085	dsRNS kinase pp68
39	3	100.0	6	21	AAB03609	Aspergillus niger
40	3	100.0	6	21	AAY84217	Amino acid sequenc
41	3	100.0	7	16	AAW21297	Glucagon precursor
42	3	100.0	7	16	AAW21304	Glucagon precursor
43	3	100.0	7	19	AAY20729	Human neurofilamen
44	3	100.0	7	20	AAY41246	Twin-arginine amin
45	3	100.0	7	20	AAY48772	Membrane dipeptida

ALIGNMENTS

RESULT 1
AAW11147
ID AAW11147 standard; peptide; 4 AA.
XX
AC AAW11147;
XX
DT 10-JUN-1997 (first entry)
XX
DE CD4 peptide capable of binding HIV gp120 to inactivate HIV.
XX
KW HIV; human immunodeficiency virus; gp120; glycoprotein 120; AIDS;
KW acquired immune deficiency syndrome; inhibit transmission.
XX
OS Synthetic.
XX
PN US5603933-A.
XX
PD 18-FEB-1997.
XX
PF 31-AUG-1993; 93US-0115171.
XX
PR 31-AUG-1993; 93US-0115171.
XX
PA (TEXA) UNIV TEXAS.
XX
PI Arlinghaus RB, Dwyer VA, Nehete PN, Sastry JK;
XX
DR WPI; 1997-144820/13.
XX
PT Compsn. comprising CD4 peptide capable of binding to HIV gp120 - for
PT protection against HIV infection
XX
PS Claim 1; Column 29; 20pp; English.
XX

```
CC   AAW11147-W11150 are CD4 peptides that bind to HIV gp120 and inactivate
CC   the virus. The peptides can be dispersed in a suitable vehicle to
CC   provide compositions useful for protecting human CD4+ cells, e.g. T
CC   cells, from HIV infection, e.g. to inhibit transmission of HIV during
CC   sexual contact. They could also be used in e.g. surgical gloves and
CC   liquid soap in hospitals to prevent HIV transmission. Alternatively, the
CC   peptides in the composition may be attached to solid supports, e.g.
CC   disposable filters, for inactivating HIV in blood and other body fluid
CC   samples.
XX
SQ   Sequence   4 AA;


  Query Match             100.0%;  Score 3;  DB 18;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SRR 3
          |||
Db      1 srr 3


RESULT   2
AAY23396
ID   AAY23396 standard; Peptide; 4 AA.
XX
AC   AAY23396;
XX
DT   02-SEP-1999  (first entry)
XX
DE   V beta 6 clone found in MS patients after vaccination with TCR.
XX
KW   Vaccine; T cell receptor; TCR; T cell; V beta 6.2/3; V beta 6/5;
KW   V beta 6.7; V beta 2; V beta 5/1; V beta 7; V beta 13; V beta 6;
KW   multiple sclerosis.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9927957-A1.
XX
PD   10-JUN-1999.
XX
PF   03-DEC-1997;   97WO-US23147.
XX
PR   03-DEC-1997;   97WO-US23147.
XX
PA   (IMMU-) IMMUNE RESPONSE CORP.
PA   (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
PI   Brostoff SW,  Carlo DJ,  Gold DP,  Smith LR,  Wilson DB;
XX
DR   WPI; 1999-404801/34.
XX
PT   T0 cell receptor peptide-derived vaccines
XX
PS   Example 11; Page 84; 104pp; English.
XX
CC   The specification describes vaccines which comprise immunologically
CC   effective amounts of T cell receptor (TCR) peptides. The TCRs are
CC   present on the surface of T cells. The TCRs are chosen from V beta
CC   6.2/3, V beta 6/5, V beta 6.7, V beta 2, V beta 5/1, V beta 7 or V beta
CC   13. The V beta TCR peptide-based vaccines are useful for prevention or
CC   treatment of multiple sclerosis (MS). The presence of V beta 6.7 appears
CC   to be particularly associated with multiple sclerosis and can be used
CC   to determine an individual's susceptibility to multiple sclerosis.
CC   Vaccinating, rather than passively administering heterologous
CC   antibodies, allows the host's own immune system to mobilize and suppress
CC   auto aggressive T cells.  Therefore, the suppression is persistent and
CC   may involve any and all immunological mechanisms in effecting that
CC   suppression.  Such a multi-faceted response is more
CC   the uni-dimensional
CC   AAY23387-Y23480 represent peptides derived from TCR V beta 6 clones
CC   found in the cerebrospinal fluid (CFS) of MS patients, after vaccination
CC   with V beta 6.
XX
SQ   Sequence   4 AA;


  Query Match             100.0%;  Score 3;  DB 20;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SRR 3
          |||
Db      1 srr 3


RESULT   3
AAB80641
ID   AAB80641 standard; peptide; 4 AA.
XX
AC   AAB80641;
XX
DT   02-MAY-2001  (first entry)
XX
DE   Human glandular kallikrein 2 cleavage site peptide #2.
XX
KW   Cleavage; kallikrein 2; hK2; prodrug.
XX
OS   Synthetic.
XX
PN   WO200109165-A2.
XX
PD   08-FEB-2001.
XX
PF   28-JUL-2000; 2000WO-US40496.
XX
PR   29-JUL-1999;   99US-0146316.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Denmeade SR,  Isaacs JT,  Lilja H,  Christensen SB;
XX
DR   WPI; 2001-191450/19.
XX
PT   New peptides containing cleavage sites specifically cleaved by human
PT   kallikrein 2, useful for producing prodrugs which treat hK2-producing
PT   cell proliferative disorders without exhibiting non-specific toxicity
PT   -
XX
PS   Disclosure; Page 7; 38pp; English.
XX
CC   The present invention relates to a peptide comprising an amino acid
CC   sequence having a cleavage site specific for an enzyme having a
CC   proteolytic activity of human kallikrein 2 (hK2), and which is up to
CC   20 amino acids in length. The invention is useful for producing a
CC   prodrug which involves linking a drug which contains a primary amine
CC   to the peptide, in which the linking of the peptide to the drug
CC   inhibits the therapeutic activity of the drug.
XX
SQ   Sequence   4 AA;


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Db      2 srr 4
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PN JP3015886-B1.
XX
PD 06-MAR-2000.
XX
PF 04-NOV-1998; 98JP-0327536.
XX
PR 04-NOV-1998; 98JP-0327536.
XX
PA (NORQ) NORINSUISANSHO SHOKUHIN SOGO.
XX
DR WPI; 2000-342275/30.
XX
PT Quick assay method of specific end protease activity of asparagine
PT residue of plant origin, involves distributing 7-methoxy
PT coumarin-4-yl-acetyl and 2,4-dinitrophenyl group to N-terminal side and
PT C-terminal side -
XX
PS Claim 1; Page 8; 11pp; Japanese.
XX
CC This sequence represents a peptide recognised and cleaved by asparagine
CC protease. The invention relates to a quick assay method for asparagine
CC protease of plant origin. The asparagine protease specifically recognises
CC asparagine residues and cleaves proteins at the C-terminal end of the
CC asparagine residue. The assay uses a fluorescence substrate (which has
CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl
CC group to the amino group of the glycine residue at the N-terminal side,
CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid
CC sequence. The fluorescence caused by the fluorescence substrate is not
CC connected to the asparagine residue and can be measured after cleavage by
CC the protease. The method is useful for assaying asparagine proteases of
CC plant origin. The activity of the protease can be determined within a
CC short time period and the enzyme activity can be measured with high
CC sensitivity using the fluorescence substrate. The procedure is quick even
CC when materials which inhibit other protease and fluorescence are included
CC in the sample.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 5; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKSRR 5
|||||
Db 1 gksrr 5

RESULT 5
AAY81916
ID AAY81916 standard; peptide; 11 AA.
XX
AC AAY81916;
XX
DT 23-JUN-2000 (first entry)
XX
DE Asparagine protease recognition peptide.
XX
KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;
KW plant protease.
XX
OS Glycine max.
XX
PN JP3015886-B1.
XX
PD 06-MAR-2000.
XX
PF 04-NOV-1998; 98JP-0327536.
XX
PR 04-NOV-1998; 98JP-0327536.
XX
PA (NORQ) NORINSUISANSHO SHOKUHIN SOGO.
XX
DR WPI; 2000-342275/30.
XX
PT Quick assay method of specific end protease activity of asparagine
PT residue of plant origin, involves distributing 7-methoxy
PT coumarin-4-yl-acetyl and 2,4-dinitrophenyl group to N-terminal side and
PT C-terminal side -
XX
PS Claim 1; Page 8; 11pp; Japanese.
XX
CC This sequence represents a peptide recognised and cleaved by asparagine
CC protease. The invention relates to a quick assay method for asparagine
CC protease of plant origin. The asparagine protease specifically recognises
CC asparagine residues and cleaves proteins at the C-terminal end of the
CC asparagine residue. The assay uses a fluorescence substrate (which has
CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl
CC group to the amino group of the glycine residue at the N-terminal side,
CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid
CC sequence. The fluorescence caused by the fluorescence substrate is not
CC connected to the asparagine residue and can be measured after cleavage by
CC the protease. The method is useful for assaying asparagine proteases of
CC plant origin. The activity of the protease can be determined within a
CC short time period and the enzyme activity can be measured with high
CC sensitivity using the fluorescence substrate. The procedure is quick even
CC when materials which inhibit other protease and fluorescence are included
CC in the sample.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 5; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKSRR 5
|||||
Db 1 gksrr 5

RESULT 6
AAY81917
ID AAY81917 standard; peptide; 11 AA.
XX
AC AAY81917;
XX
DT 23-JUN-2000 (first entry)
XX
DE Asparagine protease recognition peptide.
XX
KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;
KW plant protease.
XX
OS Glycine max.
XX
PN JP3015886-B1.
XX
PD 06-MAR-2000.
XX
PF 04-NOV-1998; 98JP-0327536.
XX
PR 04-NOV-1998; 98JP-0327536.
XX
PA (NORQ) NORINSUISANSHO SHOKUHIN SOGO.
XX
DR WPI; 2000-342275/30.
XX
PT Quick assay method of specific end protease activity of asparagine
PT residue of plant origin, involves distributing 7-methoxy
PT coumarin-4-yl-acetyl and 2,4-dinitrophenyl group to N-terminal side and
PT C-terminal side -
XX
PS Claim 1; Page 8; 11pp; Japanese.
XX
CC This sequence represents a peptide recognised and cleaved by asparagine

GenCore version 4.5

OM protein - protein search, using sw model

Run on: August 13, 2001, 11:29:55 ; Search time 58.4 Seconds
(without alignments)
1.410 Million cell updates/sec

Title: PCT-US00-40496-40
Perfect score: 4
Sequence: 1 AKRL 4

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 197339 seqs, 20590346 residues

Word size : 0

Total number of hits satisfying chosen parameters: 104997

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	4	100.0	12	2	US-08-973-563A-33	Sequence 33, Appl
4	4	100.0	12	2	US-08-973-559-33	Sequence 33, Appl
5	4	100.0	14	1	US-07-968-781A-17	Sequence 17, Appl
6	4	100.0	14	1	US-08-232-453A-6	Sequence 6, Appli
7	4	100.0	16	4	US-08-669-286-8	Sequence 8, Appli
8	4	100.0	16	4	US-09-469-253-8	Sequence 8, Appli
9	4	100.0	17	6	5304631-5	Patent No. 5304631
10	3	75.0	4	1	US-08-460-343B-67	Sequence 67, Appl
11	3	75.0	4	1	US-08-398-028B-67	Sequence 67, Appl
12	3	75.0	4	2	US-08-504-265B-67	Sequence 67, Appl
13	3	75.0	4	2	US-08-504-265B-86	Sequence 86, Appl
14	3	75.0	4	2	US-08-504-265B-87	Sequence 87, Appl
15	3	75.0	4	2	US-08-545-562A-65	Sequence 65, Appl
16	3	75.0	4	3	US-08-888-381-4	Sequence 4, Appli
17	3	75.0	4	5	PCT-US94-07779-16	Sequence 16, Appl
18	3	75.0	5	1	US-08-448-736-12	Sequence 12, Appl
19	3	75.0	5	1	US-08-452-779-12	Sequence 12, Appl
20	3	75.0	5	2	US-08-445-065-13	Sequence 13, Appl
21	3	75.0	5	3	US-08-335-733D-90	Sequence 90, Appl
22	3	75.0	5	3	US-08-959-524-13	Sequence 13, Appl
23	3	75.0	6	2	US-08-928-958-6	Sequence 6, Appli
24	3	75.0	6	2	US-09-072-429-6	Sequence 6, Appli
25	3	75.0	6	3	US-08-718-904-39	Sequence 39, Appl
26	3	75.0	6	4	US-09-177-249-214	Sequence 214, App
27	3	75.0	6	5	PCT-US95-10973A-75	Sequence 75, Appl
28	3	75.0	7	1	US-08-240-514-14	Sequence 14, Appl
29	3	75.0	7	2	US-08-612-302A-14	Sequence 14, Appl
30	3	75.0	7	2	US-08-680-326-92	Sequence 92, Appl
31	3	75.0	7	4	US-09-190-964-1	Sequence 1, Appli
32	3	75.0	7	4	US-09-190-964-3	Sequence 3, Appli
33	3	75.0	7	4	US-09-190-964-6	Sequence 6, Appli
34	3	75.0	7	4	US-09-190-964-23	Sequence 23, Appl
35	3	75.0	7	4	US-09-190-964-26	Sequence 26, Appl
36	3	75.0	7	4	US-09-190-964-27	Sequence 27, Appl
37	3	75.0	7	4	US-09-190-964-28	Sequence 28, Appl
38	3	75.0	7	4	US-09-190-964-29	Sequence 29, Appl
39	3	75.0	7	4	US-09-190-964-30	Sequence 30, Appl
40	3	75.0	7	4	US-09-100-930A-20	Sequence 20, Appl
41	3	75.0	7	5	PCT-US92-10621-50	Sequence 50, Appl
42	3	75.0	7	5	PCT-US93-12679-29	Sequence 29, Appl
43	3	75.0	7	5	PCT-US94-01234-48	Sequence 48, Appl
44	3	75.0	7	5	PCT-US94-02233-50	Sequence 50, Appl
45	3	75.0	8	2	US-08-504-265B-89	Sequence 89, Appl

ALIGNMENTS

4

RESULT 1
US-09-016-366A-50
; Sequence 50, Application US/09016366A
; Patent No. 5955431
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; APPLICANT: Huang, Chifu
; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,366A
; FILING DATE: January 30, 1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,090
; FILING DATE: 05-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-016-366A-50

Query Match 100.0%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AKRL 4
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Db      3 AKRL 6


RESULT   2
US-08-633-760-7
; Sequence 7, Application US/08633760
; Patent No. 5804429
;  GENERAL INFORMATION:
;    APPLICANT:  NIWA, MINEO
;    APPLICANT:  SAITO, YOSHIMASA
;    APPLICANT:  FUJIMURA, TAKAO
;    APPLICANT:  ISHII, YOSHINORI
;    APPLICANT:  NOGUCHI, YUJI
;    TITLE OF INVENTION:  A NEW CEPHALOSPORIN C ACYLASE
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
;      CITY:  ARLINGTON
;      STATE:  VIRGINIA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/633,760
;      FILING DATE:  01-MAY-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  18-929-0 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-633-760-7


  Query Match             100.0%;  Score 4;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AKRL 4
          ||||
Db      4 AKRL 7


RESULT   3
US-08-973-563A-33
; Sequence 33, Application US/08973563A
; Patent No. 5885965
;  GENERAL INFORMATION:
;    APPLICANT:  Oppenheim, Frank G.
;    APPLICANT:  Xu, Tao
;    APPLICANT:  Spacciapoli, Peter
;    APPLICANT:  Roberts, F. D.
;    APPLICANT:  Friden, Philip M.
;    TITLE OF INVENTION:  Anti-Fungal D-Amino Acid Histatin-Based
;    TITLE OF INVENTION:  Peptides
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/973,563A
;      FILING DATE:  07-JUN-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/485,273
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook, David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  PER95-02A2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  781-861-6240
;      TELEFAX:  781-861-9540
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Region
;      LOCATION:  1..12
;      OTHER INFORMATION:  /note= "At least one amino acid
;      OTHER INFORMATION:  must have a D configuration."
US-08-973-563A-33


  Query Match             100.0%;  Score 4;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AKRL 4
          ||||
Db      1 AKRL 4


RESULT   4
US-08-973-559-33
; Sequence 33, Application US/08973559
; Patent No. 5912230
;  GENERAL INFORMATION:
;    APPLICANT:  OPPENHEIM, FRANK G.
;    APPLICANT:  XU, TAO
;    APPLICANT:  ROBERTS, F. D.
;    APPLICANT:  SPACCIAPOLI, PETER
;    APPLICANT:  FRIDEN, PHILIP M.
;    TITLE OF INVENTION:  Anti-Fungal and Anti-Bacterial
;    TITLE OF INVENTION:  Histatin-Based Peptides
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02173
;    COMPUTER READABLE FORM:
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